## SEQUENCE LISTING

<110> IMAEDA, TAKAO YAMADA, YUKIO HIRAI, MASANA SHIMAMURA, TAKASHI KOHDA, KATSUNORI MURAMOTO, NOBUHIKO <120> METHOD FOR PRODUCING ANTIMICROBIAL PROTEIN AND FUSION PROTEIN 130> 208377US0 150> JP2000-161090 <151> 2000-05-26 J. <u></u> 160> 12 I,F 170> PatentIn version 3.0 <210> 1 <211> 392 <212> DNA <213> Hordeum vulgare <220> <221> CDS <222> (1)..(390) <400> 1

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Glu Lys His Met Ile Glu Gly Arg Met Lys Ser Cys Cys Arg Ser Thr

48

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Leu Cys Ala Gly Val Cys Arg Cys Lys Leu Thr Ser Ser Gly Lys Cys 35 40 45

Pro Thr Gly Phe Pro Lys Met Ile Glu Gly Arg Thr Leu Ala Leu Val 55 Ser Asn Ser Asp Glu Pro Asp Thr Val Lys Tyr Cys Asn Leu Gly Cys Arg Ala Ser Met Cys Asp Tyr Met Val Asn Ala Ala Ala Asp Asp Glu Glu Met Lys Leu Tyr Leu Glu Asn Cys Gly Asp Ala Cys Val Asn Phe 105 Cys Asn Gly Asp Ala Gly Leu Thr Ser Leu Thr Ala 120 <210> **211**> © (**212**> PRT 213> Hordeum vulgare .... ijħ **400> 3** Asp Pro Ala Ala "L Z210> <211> 1649 <212> DNA <213> Hordeum vulgare <220> <221> CDS <222> (1)..(1647) <400> 4

gac aag cat atg att gaa ggt cgt aaa agc tgc tgc cgt agc acc ctg Asp Lys His Met Ile Glu Gly Arg Lys Ser Cys Cys Arg Ser Thr Leu 1 5 10 15 48

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ggt	aat	226	taa	+ > +	224	at a	taa	cat	at t	cat	aat	aca	C2C	222	cta	96
Gly .	_		_			_	_	_	_	-			-		-	96
tgc Cys																144
acc Thr																192
aag Lys 65					gac Asp 70											240
					ccg Pro											288
Glu					gcg Ala											336
gcc Ala	aag Lys	gtg Val 115	gac Asp	tgc Cys	aca Thr	gag Glu	gag Glu 120	acg Thr	gac Asp	ctc Leu	tgc Cys	caa Gln 125	caa Gln	cat His	ggt Gly	384
gtt Val				_												432
tcc Ser 145	ccc Pro	tac Tyr	aag Lys	ggc	cag Gln 150	cgc Arg	aag Lys	gct Ala	gct Ala	gct Ala 155	Ile	acc Thr	tcg Ser	tac Tyr	atg Met 160	480
atc =Ile	aag Lys	cag Gln	tct Ser	ctg Leu 165	ccc Pro	gcc Ala	gtg Val	tcc Ser	gag Glu 170	gtc Val	acg Thr	aag Lys	gac Asp	aac Asn 175	ctg Leu	528
					gcc Ala				Val							576
			Lys					Val					Ala		aag Lys	624
_	_	Asp			_		gly		_	-		Āla			gcc Ala	672
	Ala					Ala					. Let				ttt Phe 240	720
					Val					Phe					atc Ile	768

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											ctc Leu						8	16
		_				_		-	_	_	ggc Gly			_	_		8	864
											gag Glu						9	912
I											att Ile 315						9	960
~		_	_	_			_		_		aac Asn	_		_	-		10	800
	ga	Lys	Phe	Pro 340	Āla	Phe	Āla	Ile	Gln 345	Glu	gtc Val	Āla	Lys	Asn 350	Gln	Lys	10	056
io t ii p	tc he	ccc Pro	ttc Phe 355	gat Asp	cag Gln	gag Glu	aag Lys	gag Glu 360	atc Ile	acc Thr	ttc Phe	gag Glu	gcg Ala 365	atc Ile	aag Lys	gct Ala	11	L04
in t	tc he	gtc Val 370	gac Asp	gac Asp	ttt Phe	gtc Val	gcc Ala 375	ggt Gly	aag Lys	atc Ile	gag Glu	ccc Pro 380	agc Ser	atc Ile	aag Lys	tcg Ser	11	152
	27 22										gtc Val 395						12	200
13 e											acc Thr						12	248
								ĞÎy		Cys	aag Lys						1:	296
														Lys		cgg Arg	1	344
																gag Glu	1	392
		Gln					Ile					Ala				ggt Gly 480	1	440
						Ser					Val					aag Lys	1	488

		gcc														153	6
Phe	Ile	Ala	Glu 500	Asn	Gly	Lys	Tyr	Lys 505	Ala	Ala	Ile	Ser	Glu 510	Asp	Ala		
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Cys	Ala	Gly 35	Val	Cys	Arg	Cys	Lys 40	Leu	Thr	Ser	Ser	Gly 45	Lys	Cys	Pro		
Thr	Gly 50	Phe	Pro	Lys	Met	Ile 55	Glu	Gly	Arg	Ser	Asp 60	Val	Val	Gln	Leu		
Lys 65	Lys	Asp	Thr	Phe	Asp 70	Asp	Phe	Ile	Lys	Thr 75	Asn	Asp	Leu	Val	Leu 80		
Ala	Glu	. Phe	Phe	Ala 85	Pro	Trp	Cys	Gly	His 90	Cys	Lys	Ala	Leu	Ala 95	Pro		
Glu	Туг	Glu	Glu 100		Ala	Thr	Thr	Leu 105		Glu	Lys	Asn	Ile 110	_	Leu		
Ala	Lys	Val 115	_	Cys	Thr	Glu	Glu 120		· Asp	Leu	Cys	Gln 125		His	Gly		

Val Glu Gly Tyr Pro Thr Leu Lys Val Phe Arg Gly Leu Asp Asn Val 130 135 140

Ser Pro Tyr Lys Gly Gln Arg Lys Ala Ala Ala Ile Thr Ser Tyr Met 145 150 155 160

Ile Lys Gln Ser Leu Pro Ala Val Ser Glu Val Thr Lys Asp Asn Leu 165 170 175

Glu Glu Phe Lys Lys Ala Asp Lys Ala Val Leu Val Ala Tyr Val Asp 180 185 190

Ala Ser Asp Lys Ala Ser Ser Glu Val Phe Thr Gln Val Ala Glu Lys 195 200 205

Leu Arg Asp Asn Tyr Pro Phe Gly Ser Ser Ser Asp Ala Ala Leu Ala 210 215 220

Glu Ala Glu Gly Val Lys Ala Pro Ala Ile Val Leu Tyr Lys Asp Phe 225 230 235 240

Asp Glu Gly Lys Ala Val Phe Ser Glu Lys Phe Glu Val Glu Ala Ile
245 250 255

Glu Lys Phe Ala Lys Thr Gly Ala Thr Pro Leu Ile Gly Glu Ile Gly 260 265 270

11

Pro Glu Thr Tyr Ser Asp Tyr Met Ser Ala Gly Ile Pro Leu Ala Tyr 275 280 285

Ile Phe Ala Glu Thr Ala Glu Glu Arg Lys Glu Leu Ser Asp Lys Leu 290 295 300

Lys Pro Ile Ala Glu Ala Gln Arg Gly Val Ile Asn Phe Gly Thr Ile 305 310 315 320

Asp Ala Lys Ala Phe Gly Ala His Ala Gly Asn Leu Asn Leu Lys Thr 325 330 335

Asp Lys Phe Pro Ala Phe Ala Ile Gln Glu Val Ala Lys Asn Gln Lys 340 345 350

Phe Pro Phe Asp Gln Glu Lys Glu Ile Thr Phe Glu Ala Ile Lys Ala 355 360 365

Phe Val Asp Asp Phe Val Ala Gly Lys Ile Glu Pro Ser Ile Lys Ser 370 380

Glu Pro Ile Pro Glu Lys Gln Glu Gly Pro Val Thr Val Val Val Ala 385 390 395 400

Lys Asn Tyr Asn Glu Ile Val Leu Asp Asp Thr Lys Asp Val Leu Ile 405 410 415

Glu Phe Tyr Ala Pro Trp Cys Gly His Cys Lys Ala Leu Ala Pro Lys
420 425 430

Tyr Glu Glu Leu Gly Ala Leu Tyr Ala Lys Ser Glu Phe Lys Asp Arg 435 440 445

Val Val Ile Ala Lys Val Asp Ala Thr Ala Asn Asp Val Pro Asp Glu 450 455 460

The Gln Gly Phe Pro Thr Ile Lys Leu Tyr Pro Ala Gly Ala Lys Gly

In Pro Val Thr Tyr Ser Gly Ser Arg Thr Val Glu Asp Leu Ile Lys
485
490
495

The Ile Ala Glu Asn Gly Lys Tyr Lys Ala Ala Ile Ser Glu Asp Ala
500 505 510

Glu Glu Thr Ser Ser Ala Thr Glu Thr Thr Glu Thr Ala Thr Lys 515 520 525

Ser Glu Glu Ala Ala Lys Glu Thr Ala Thr Glu His Asp Glu Leu 530 535 540

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Leu Cys Ala Gly Val Cys Arg Cys Lys Leu Thr Ser Ser Gly Lys Cys

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       DNA
      Hordeum vulgare
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                                                                      48
Asp Lys His Met Ile Glu Gly Arg Lys Ser Cys Cys Arg Ser Thr Leu
ggt cgt aac tgc tat aac ctg tgc cgt gtt cgt ggt gcg cag aaa ctg
                                                                       96
Gly Arg Asn Cys Tyr Asn Leu Cys Arg Val Arg Gly Ala Gln Lys Leu
            20
tgc gcg ggt gtt tgc cgt tgc aaa ctg acc agc ggt aaa tgc ccg
                                                                      144
Cys Ala Gly Val Cys Arg Cys Lys Leu Thr Ser Ser Gly Lys Cys Pro
        35
acc ggt ttt ccg aaa atg att gaa ggt cgt gag acg tcg tcc gca acc
                                                                      192
Thr Gly Phe Pro Lys Met Ile Glu Gly Arg Glu Thr Ser Ser Ala Thr
    50
gag acg acc acc gag acg gcc acc aag tcg gag gag gct gcc aag gag
                                                                      240
Glu Thr Thr Thr Glu Thr Ala Thr Lys Ser Glu Glu Ala Ala Lys Glu
65
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284

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<211> 88

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Cys Ala Gly Val Cys Arg Cys Lys Leu Thr Ser Ser Gly Lys Cys Pro 35 40 45

Thr Gly Phe Pro Lys Met Ile Glu Gly Arg Glu Thr Ser Ser Ala Thr 50 55 60

GTu Thr Thr Glu Thr Ala Thr Lys Ser Glu Glu Ala Ala Lys Glu 65 70 75 80

Thr Ala Thr Glu His Asp Glu Leu

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<213> Hordeum vulgare

<400> 12

Asp Pro Ala Ala